

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:32:18 : Search time 10 Seconds
(without alignments)
2086.259 Million cell updates/sec

Title: US-10-025-514-16

Perfect score: 2675

Sequence: 1 MEDPQDAAQKDTSHHDQD.....RDLKCCMGKSCVSPVKA 503

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2030	75.9	418	1	ALAT_HUMAN
2	1894	70.8	409	1	ALAT_PAPAN
3	1491.5	55.8	412	1	ALAT_CALCN
4	1486.5	55.6	421	1	ALAT_PIG
5	1455.5	54.4	411	1	ALAT_RAT
6	1455	54.4	416	1	ALAT_SHEEP
7	1436	53.7	413	1	ALMM_TAMSI
8	1434	53.6	416	1	ALAT_BOVIN
9	1392	52.0	413	1	ALST_TAMSI
10	1388	51.9	413	1	ALSI_TAMSI
11	1376	51.4	413	1	ALMS_TAMSI
12	1338	50.0	413	1	ALAF_RABIT
13	1335	49.9	413	1	ALTI_MOUSE
14	1333	49.8	413	1	ALT2_MOUSE
15	1329	49.7	413	1	ALT3_MOUSE
16	1321	49.4	413	1	HP55_TAMSI
17	1316	49.2	413	1	ALT4_MOUSE
18	1302	48.7	413	1	ALT5_MOUSE
19	1295.5	48.4	412	1	ALAT_MUSCR
20	1293	48.3	405	1	ALAS_CAVPO
21	1266	47.3	403	1	ALAF_CAVPO
22	1246	46.6	410	1	COTR_CAVPO
23	1158.5	43.3	410	1	ALAT_DIDMA
24	1140	42.6	420	1	ALAU_HUMAN
25	849	31.7	423	1	AACT_HUMAN
26	829	31.0	418	1	COTR_MOUSE
27	816	30.5	406	1	CBG_SATSC
28	816	30.5	406	1	IPSP_HUMAN
29	816	30.5	418	1	CP16_RAT
30	816	30.5	427	1	KATN_HUMAN
31	815.5	30.5	405	1	CBG_HUMAN
32	812.5	30.4	416	1	CP11_RAT
33	811	30.3	393	1	CBG_RABIT

34 805 30.1 430 1 CBG_SHEEP
35 804 30.1 417 1 KBP_MOUSE
36 803 30.0 413 1 CP13_RAT
37 799.5 29.9 412 1 THBG_PIG
38 787.5 29.4 415 1 THBG_HUMAN
39 786.5 29.4 412 1 THBG_SHEEP
40 782.5 29.3 411 1 THBG_BOVIN
41 774.5 29.0 409 1 THBG_RAT
42 771.5 28.8 405 1 IPSP_MOUSE
43 771.5 28.8 418 1 SI24_APOSY
44 739 27.6 372 1 ALAT_CYPCA
45 720.5 26.9 397 1 CBG_MOUSE

ALIGNMENTS

RESULT 1
ALAT_HUMAN
ID ALAT_HUMAN STANDARD; PRT; 418 AA.
AC P01009; QSP1P0; Q13672;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE antiprotease) (PRO0684/PRO2209).
GN SERPINAL OR PI OR AAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84107980; PubMed=6319097;
RA Bollin A., Herzog A., Cravador A., Herion P., Chuchana P.,
RA van der Straten A., Loxiau R., Jacobs P., van Elsen A.;
RT "Cloning and expression in Escherichia coli of full-length
RT complementary DNA coding for human alpha 1-antitrypsin.";
RL DNA 2:255-264 (1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85036645; PubMed=6387509;
RA Rosenberg S., Barr P.J., Najarian R.C., Hallelwell R.A.;
RT "Synthesis in yeast of a functional oxidation-resistant mutant of
RT human alpha-antitrypsin.";
RL Nature 312:77-80(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85047190; PubMed=6093867;
RA Long G.L., Chandra T., Woo S.L.C., Davie E.W., Kurachi K.;
RT "Complete sequence of the cDNA for human alpha 1-antitrypsin and the
RT gene for the S variant.";
RL Biochemistry 23:4828-4837(1984).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS 2.
RX MEDLINE=87057257; PubMed=3491072;
RA Nukiwa T., Satoh K., Brantly M.L., Ogushi F., Fells G.A.,
RA Courtney M., Crystal R.G.;
RT "Identification of a second mutation in the protein-coding sequence
RT of the Z type alpha 1-antitrypsin gene.";
RL J. Biol. Chem. 261:15989-15994(1986).
RN [5]
RP ERRATUM.
RA Nukiwa T., Satoh K., Brantly M.L., Ogushi F., Fells G.A.,
RA Courtney M., Crystal R.G.;
RL J. Biol. Chem. 262:10412-10412(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=85176977; PubMed=2985281;
RA Ciliberto G., Dente L., Cortese R.;
RT "Cell-specific expression of a transfected human alpha 1-antitrypsin
RT gene.";
RL Cell 41:531-540(1985).

- RN [7] SEQUENCE FROM N.A.
RP
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
RT Zhou W., Bi J., Zhang Y., Liu M., He F.;
RA "Functional prediction of the coding sequences of 32 new genes deduced
RT by analysis of cDNA clones from human fetal liver.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RA Vaughan L., Boswell D.R.;
RT "Structure and variation of human alpha 1-antitrypsin.";
RL Nature 298:329-334(1982).
RN [9]
RP PRELIMINARY SEQUENCE OF 25-418.
RA Chan S.K.;
RT "The covalent structure of human alpha1-protease inhibitor.";
RL Fed. Proc. 41:1016-1016(1982).
RN [10]
RP SEQUENCE OF 1-67; 196-255 AND 387-418 FROM N.A.
RX MEDLINE=82220035; PubMed=6979715;
RA Leicht M., Long G.L., Chandra T., Kurachi K., Kidd V.J., Mace M. Jr.,
RA Davie E.W., Woo S.L.C.;
RT "Sequence homology and structural comparison between the chromosomal
RT human alpha 1-antitrypsin and chicken ovalbumin genes.";
RL Nature 297:655-659(1982).
RN [11]
RP SEQUENCE OF 291-418 FROM N.A.
RX MEDLINE=86005469; PubMed=7031661;
RA Riley J.H., Bathurst I.C., Edbrooke M.R., Carrell R.W., Craig R.K.;
RT "Alpha 1-antitrypsin and serum albumin mRNA accumulation in normal,
RT acute phase and ZZ human liver.";
RL FEBS Lett. 189:361-366(1985).
RN [12]
RP SEQUENCE OF 350-418 FROM N.A.
RX MEDLINE=84292309; PubMed=6332197;
RA Kurachi K., Chandra T., Friezeher Degen S.J., White T.T.,
RA Marchioro T.L., Woo S.L.C., Davie E.W.;
RT "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
RN [13]
RP SEQUENCE OF 387-418 FROM N.A.
RX MEDLINE=85225507; PubMed=3873938;
RA Coutelle C., Speer A., Rogers J., Kalsheker N., Humphries S.,
RA Williamson R.;
RT "Construction and partial characterization of a human liver cDNA
RT library.";
RL Biomed. Biochim. Acta 44:421-431(1985).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=84292309; PubMed=6332197;
RA Loebermann H., Tokuda R., Deisenhofer J., Huber R.;
RT "Human alpha 1-proteinase inhibitor. Crystal structure analysis of
RT two crystal modifications, molecular model and preliminary analysis
RT of the implications for function.";
RL J. Mol. Biol. 177:531-556(1984).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=89221004; PubMed=2785270;
RA Engh R., Loebermann H., Schneider M., Wiegand G., Huber R.,
RA Laurell C.-B.;
RT "The S variant of human alpha 1-antitrypsin, structure and
RT implications for function and metabolism.";
RL Protein Eng. 2:407-415(1989).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=20386623; PubMed=10933492;
RA Elliott P.R., Pei X.Y., Dafforn T.R., Lomas D.A.;
RT "Topography of a 2.0 A structure of alpha1-antitrypsin reveals targets
RT for rational drug design to prevent conformational disease.";
RL Protein Sci. 9:1274-1281(2000).
RN [17]
RP REVIEW.
RX MEDLINE=89352843; PubMed=2669992;
RA Kalsheker N.;
RT "Alpha 1-antitrypsin: structure, function and molecular biology of
RT the gene.";
RL Biosci. Rep. 9:129-138(1989).
RN [18]
RP REVIEW.
RX MEDLINE=91315455; PubMed=1859394;
RA Wu Y., Foreman R.C.;
RT "The molecular genetics of alpha 1 antitrypsin deficiency.";
RL Bioessays 13:163-169(1991).
RN [19]
RP VARIANT M2.
RX MEDLINE=88324438; PubMed=2901226;
RA Nukiwa T., Brantly M.L., Ogushi F., Fells G.A., Crystal R.G.;
RT "Characterization of the gene and protein of the common alpha 1-
RT antitrypsin normal M2 allele.";
RL Am. J. Hum. Genet. 43:322-330(1988).
RN [20]
RP VARIANT M3.
RX MEDLINE=90368097; PubMed=2394452;
RA Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.F.,
RA Kalsheker N.A.;
RT "Characterisation of the alpha-1-antitrypsin M3 gene, a normal
RT variant.";
RL Hum. Genet. 85:381-382(1990).
RN [21]
RP VARIANT F.
RX MEDLINE=91241132; PubMed=2035534;
RA Okayama H., Brantly M., Holmes M., Crystal R.G.;
RT "Characterization of the molecular basis of the alpha 1-antitrypsin F
RT allele.";
RL Am. J. Hum. Genet. 48:1154-1158(1991).
RN [22]
RP VARIANT M-HEERLEN.
RX MEDLINE=89154435; PubMed=2784123;
RA Hofker M.H., Nukiwa T., van Paassen H.M.B., Nelen M., Kramps J.A.,
RA Klase E.C., Frants R.R., Crystal R.G.;
RT "A Pro-->Leu substitution in codon 369 of the alpha-1-antitrypsin
RT deficiency variant PI M-Heerlen.";
RL Hum. Genet. 81:264-268(1989).
RN [23]
RP VARIANT M-MALTON.
RX MEDLINE=89270478; PubMed=2786335;
RA Fraizer G.C., Harrold T.R., Hofker M.H., Cox D.W.;
RT "In-frame single codon deletion in the M-Malton deficiency allele of
RT alpha 1-antitrypsin.";
RL Am. J. Hum. Genet. 44:894-902(1989).
RN [24]
RP VARIANT M-MINERAL SPRINGS.
RX MEDLINE=90097863; PubMed=1967187;
RA Curiel D.T., Vogelmeier C., Hubbard R.C., Stier L.E., Crystal R.G.;
RT "Molecular basis of alpha 1-antitrypsin deficiency and emphysema
RT associated with the alpha 1-antitrypsin M-Mineral springs allele.";
RL Mol. Cell. Biol. 10:47-56(1990).
RN [25]
RP VARIANT M-NICHINAN.
RX MEDLINE=90178096; PubMed=2309708;
RA Matsunaga E., Shiohara S., Nakamura H., Maruyama T., Tsuda K.,
RA Fukumaki Y.;
RT "Molecular analysis of the gene of the alpha 1-antitrypsin deficiency
RT variant, M-Nichinan.";
RL Am. J. Hum. Genet. 46:602-612(1990).
RN [26]
RP VARIANT M-PROCIDA.
RX MEDLINE=89008457; PubMed=3262617;
RA Takahashi H., Nukiwa T., Satoh K., Ogushi F., Brantly M., Fells G.,
RA Stier L., Courtney M., Crystal R.G.;
RT "Characterization of the gene and protein of the alpha 1-antitrypsin
RT 'deficiency' allele M-Procida.";
RL J. Biol. Chem. 263:15528-15534(1988).

CC -I- FUNCTION: INHIBITOR OF SERINE PROTEASES (By similarity).

Db	196	VFALVNYIFFKGWERPFVEATEEEDHFVDQATTVKVPMRRRLGMFNITYHCEKLSSWVL	255
Qy	242	LMKYLGNATAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITCTGYDLK	301
Db	256	LMKYLGNATAIFFLPDEGKLOHLENELTHDIIITKFLNENRRRSANJHLPKLAITGTYDLK	315
Qy	302	SVLZQLGKITKVFNSGADLSGVTTEAPLKLSKAVHKVAVLTIDKGTTEAAGAMFLEAIPMSI	361
Db	316	TVLGHGKITKVFNSGADLSGVTEDAPLKLSKAVHKVAVLTIDKGTTEAAGAMFLEAIPMSI	375
Qy	362	PPEVKNKPFVFLMIEQNTKSPLEFMGKVVNPOTK	395
Db	376	PPEVKNKPFVFLMIEQNTKSPLEFMGKVVNPOTK	409
RESULT 3			
ID	ALAT_CALCIN	STANDARD;	PRT; 412 AA.
AC	054763;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Alpha-1-antiproteinase precursor (Alpha-1-antitrypsin) (Alpha-1-		
OS	Proteinase inhibitor).		
OS	Callosclurus caniceps (Gray-bellied squirrel).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Scluridae; Sclurinae;		
OC	Callosclurus.		
OX	NCBI_Taxid=64664;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RC	MEDLINE=98094263; PubMed=9434174;		
RA	Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,		
RA	Tsutsu S., Watanabe M., Kondo J., Kondo N., Shiba T.;		
RT	"Expression of multiple alpha-1-antitrypsin-like genes in hibernating		
RT	species of the squirrel family.";		
RL	Gene 204:127-132(1997).		
CC	!- FUNCTION: INHIBITOR OF SERINE PROTEASES (By similarity)		

ALAT_RAT
ID ALAT_RAT STANDARD; PRT; 411 AA.
AC P17475;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-
DE protease inhibitor).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE OF 4-411 FROM N.A., AND SEQUENCE OF 25-57.
RP TISSUE=Liver;
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=90148955; PubMed=2302382;
RA Misumi Y., Sonda M., Ohkubo K., Takami N., Oda K., Ikehara Y.;
RT "Molecular cloning and sequencing of the cDNA of rat alpha 1-protease
RT inhibitor and its expression in COS-1 cells.";
RL J. Biochem. 108:230-234(1990).
RN [3]
RP SEQUENCE OF 188-389 FROM N.A.
RC TISSUE=Liver;
RA Flank I.L., Bailey T., Morkin E.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. THE PRIMARY TARGET IS
CC ELASTASE, BUT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
CC THROMBIN.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC
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CC
CC EMBL; M32247; AAA40788.1; -
CC EMBL; D00675; BAA00579.1; -
CC EMBL; X16273; CAA34349.1; -
CC PIR; A33892; ITRT.
CC HSP; P01009; 9A1.
CC InterPro; IPR00215; Serpin.
CC Pfam; PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
FT SIGNAL 1 24
FT CHAIN 25 411
FT ACT_SITE 376 377
FT ACT_SITE 376 377
FT CARBOHYD 64 64
FT CARBOHYD 101 101
FT CARBOHYD 265 265
FT CONFLICT 14 14
FT CONFLICT 84 84
FT CONFLICT 247 247
FT CONFLICT 248 248
FT CONFLICT 318 318
FT CONFLICT 322 322
FT CONFLICT 411 AA; 46135 MW; B4245CFE21C5C761 CRC64;
SQ SEQUENCE 411 AA; 46135 MW; B4245CFE21C5C761 CRC64;
Query Match 54.4%; Score 1455.5; DB 1; Length 411;
Best Local Similarity 70.2%; Pred. No. 1e-86;

Matches 271; Conservative 63; Mismatches 51; Indels 1; Gaps 1;
QY 9 AOKTDTSHDQDHPTFNKITNLAFAFSLYRQLAHOSNSTNIEFSPVSIATAFAMLSLG 68
DB 27 AQETDTSQDQS-PTYRKISSNLADAFSLYRELHVOSNTSNIEFSPMSITAFAMLSLG 85
QY 69 TKADTHDEILGLNLTETPEAOTHEGFOELLRTLNOPDSOLOLTTCNGLFLSEGLKLV 128
DB 86 SKGDTKRKQILGLLEFNLTOIPEADLHKAFHLLQTLNRPDSELOLNTGLFVNKNLKV 145
QY 129 DKFLEDVKLYHSAFTVNFQDTEBAKKQINDYVEKGTQGRIVDLVKELDRDTVFALVNY 188
DB 146 EKFLVEKNYHSAFVSFADSEAKKINDYVEKGTQGRIVDLVKELDRDTVFALVNY 205
QY 189 IFFGKWERPEFVKDTEEDFHVQVTVKVPMMKRLGMFNHIOCKKLSWVLMKYLGN 248
DB 206 IFFGKWKRPENPEHTRDADFHVQVTVKVPMMNRLGMFDMHYCSTLSSVLMMDYLG 265
QY 249 ATAIFFLPDECKLOHLENLTHDIITKFLNEDRRSASLHLPKLSITGTVDLKSVLQGL 308
DB 266 ATAIFLLPDDGKMHLEQTLTKDLISRLNQRTRAILYFPKLSISGTYNLKTLLSSLG 325
QY 309 ITKVFSGADLSGVTEEAPLKLSKAVHKAVLTIDEKTEAAGAMFLAIPMSIPEVKFN 368
DB 376 ITRVFNDDADLSGITEDAPLKLSQAVHKAVLTLDERTGAAGATVVEAVPMSLPPQVKFD 385
QY 369 KPFVFLMIEQNTKSPLEMGKVVNPQTQ 394
DB 386 HPFIFMIVESETQSPLEFVGKVIDPTR 411

RESULT 6
ALAT_SHEEP
ID ALAT_SHEEP STANDARD; PRT; 416 AA.
AC P12725;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-
DE protease inhibitor).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89366677; PubMed=2788872;
RA Brown W.M., Dziegielewska K.D., Foreman R.C., Saunders N.R., Wu Y.;
RT "Nucleotide and deduced amino acid sequence of sheep alpha 1
RT antitrypsin.";
RL Nucleic Acids Res. 17:6398-6398(1989).
RN [2]
RP SEQUENCE OF 25-55.
RC TISSUE=Plasma;
RX MEDLINE=91144555; PubMed=1899999;
RA Mistry R., Snashall P.D., Totty N., Guz A., Tetley T.D.;
RT "Isolation and characterization of sheep alpha 1-proteinase
RT inhibitor.";
RL Biochem. J. 273:685-690(1991).
CC -1- FUNCTION: INHIBITS HUMAN LEUKOCYTE ELASTASE, PIG PANCREATIC
CC ELASTASE AND BOVINE TRYPSIN ON A 1:1 MOLAR BASIS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC
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CC EMBL; X15555; CAA33561.1; -.
 CC PIR; S05312; ITSH.
 DR HSSP; P01009; 1KCT.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
 FT SIGNAL 1 24 ALPHA-1-ANTITRYPSINASE.
 FT CHAIN 25 416 REACTIVE BOND.
 FT ACT_SITE 380 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 39 39 A -> S (IN REF. 2).
 FT CONFLICT 45 45 C -> A (IN REF. 2).
 SQ SEQUENCE 416 AA; 45984 MW; 0B4702C0527321BF CRC64;

Query Match 54.48; Score 1455; DB 1; Length 416;
 Best Local Similarity 70.58; Pred. No. 1.1e-86;
 Matches 275; Conservative 59; Mismatches 54; Indels 2; Gaps 1;

QY 5 QGDAQAQTDTSHHQDHPFTFNKIPNLAFAFSLYROLAHQSNTNFIFFSPVSIATAFAM 64
 DB 28 QGHAVQETDDTAHQE--AACHKIAPNLANFAFSIYKLAHQSNISFIFFSPVSIASAFAM 85
 QY 65 LSLGKADTHDEILGLNFNLTETPEAQIHGFGQELLRTLNQPSQQLTGTGGLFSEB 124
 DB 86 LSLGAKGNTHTEILGLGNLTETLAEEAIHKGFQHLHLTLNPNHQLTGTGGLFSEB 145
 QY 125 LKLVDFKELDKVLYHSAFVNFQDTEAKKQINDVYKGTQGIYDLVKELDRDTVFA 184
 DB 146 AKLVDTFLEDVKNLHSAFVNFQDTEAKKQINDVYKGTQGIYDLVKELDRDTVFA 205
 QY 185 LVNYIFFKGKWERPEVAKDTEEDFHVQDVTYKVPMMKRLGMFNIOHCKKLSWLLMK 244
 DB 206 LVNYISFGKWKPEVEHTTDFHVNEQTYKVPMMNRLGMFMDLHYCDKLSWLLLD 265
 QY 245 YLGNATATFFLPDEKQLHLENLTHDIITKFLNEDRRSASLHLPKLSITGTVDLKSVL 304
 DB 266 YVGNVTACFILPDGLKLOLEDKLNELLAFLKFLKFKYASSANLHLPKLSITSETYDLKTVL 325
 QY 305 GOLGTTKVFSGADLSGVTEAPLKLKSAVKAVLTIDEKTEAAGAMFLEAIPMSIPPE 364
 DB 326 GELGNRVFSGADLSGVTEAPLKLKSAVKAVLTIDEKTEAAGAMFLEAIPMSIPPD 385
 QY 365 VKFNKPFVFLMEQNTKSPFLFMGVNPTQ 394
 DB 386 VEFNRPFLCYLDNRNTPKSPFLFMGVNPTQ 415

RESULT 7
 ALMM_TAMSI
 ID ALMM_TAMSI STANDARD; PRT; 413 AA.
 AC O54757;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Alpha-1-antitrypsin-like protein CM55-MM precursor.
 OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Tamias.
 OX NCBI_TaxID=64680;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98094263; PubMed=9434174;
 RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
 RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;

Expression of multiple alphas-1-antitrypsin-like genes in hibernating species of the squirrel family.;
 RT Gene 204;127-132(1997).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-ANTITRYPSIN.
 CC
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CC EMBL; AB000546; BAA24416.1; -.
 DR HSSP; P01009; 8API.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-MM.
 FT MOD_RES 25 23 PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 413 AA; 46212 MW; DIC378899BB20B69 CRC64;

Query Match 53.78; Score 1436; DB 1; Length 413;
 Best Local Similarity 70.18; Pred. No. 1.9e-85;
 Matches 270; Conservative 58; Mismatches 57; Indels 0; Gaps 0;

QY 9 AQKTDTSHHQDHPFTFNKIPNLAFAFSLYROLAHQSNTNFIFFSPVSIATAFAMLSLG 68
 DB 27 AQTEASKKQDEHPASHRIAPHLAEFALSILYRLAHQSNTNFIFFSPVSIATAFAMLSLG 86
 QY 69 TKADTDEILEGNFNLTETPEAQIHGFGQELLRTLNQPSQQLTGTGGLFSEGLKLV 128
 DB 87 TKGDTHTQILEGLDFNLTEMAEADIHGQFNLLQTLNRPNTQQLTSGNGLFIHQNLKL 146
 QY 129 DKFLEDVKKLYHSEAFVNFQDTEEAKKQINDVYKGTQGIYDLVKELDRDTVFAVNY 188
 DB 147 DKFLEDVKKLYHSEALPTNFTNTEEARQQINSYVERGTQGIYDLVKELDRDTVFAVNY 206
 QY 189 IFFKGKWERPFEVAKDTEEDFHVQDVTYKVPMMKRLGMFNIOHCKKLSWLLMKYLCN 248
 DB 207 IFFKGKWEPEFNEEDTKEDFHVDEATTVRPMNRLGMFMDLHYCDKLSWLLMDYLGN 266
 QY 249 ATAIFFLPDGKLOHLENLTHDIITKFLNEDRRSASLHLPKLSITGTVDLKSVLGQLG 308
 DB 267 ATAIFLLPDGKMQHLEDVTVMEILSKFLKRNRETLVDLVFFKVSISGTYDLKTVLHSLG 326
 QY 309 ITRVFSNGADLSGVTEAPLKLKSAVKAVLTIDEKTEAAGAMFLEAIPMSIPPEVKEN 368
 DB 327 ITRVFSQADLSGVTEAPLTVSKLHKAVALDIHEKGTDAAGATFLEIMPMLPPDKMFD 386
 QY 369 KPFVFLMEQNTKSPFLFMGVNPT 393
 DB 387 RPFVLVIYHHHTKSPFLFMGVNPT 411

RESULT 8
 ALAT_BOVIN
 ID ALAT_BOVIN STANDARD; PRT; 416 AA.
 AC P34955;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-

```
DE proteinase inhibitor).
GN PI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92223096; PubMed=1562597;
RA Slnha D., Bakshi M.R., Kirby E.P.;
RT "Complete cDNA sequence of bovine alpha 1-antitrypsin.";
RL Biochim. Biophys. Acta 1130:209-212(1992).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X63129; CAA44840.1; -.
CC PIR: S21097; S21097.
CC PIR: S18920; S18920.
CC HSP: P01009; IOLP.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART: SM00093; SERPIN; 1.
CC PROSITE: PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
KW SIGNAL
FT CHAIN 1 24
FT ACT_SITE 25 416
FT REACTIVE_BOND.
FT CARBOHYD 68 68 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 416 AA; 46104 MW; 3280CDAF42DA35E2 CRC64;
Query Match 53.6%; Score 1434; DB 1; Length 416;
Best Local Similarity 69.7%; Pred. No. 2.6e-85;
Matches 272; Conservative 58; Mismatches 58; Indels 2; Gaps 1;
QY 5 QGDAQAQTSDDHDDHPTNKTPNLAEPFSLYROLAHQSNSTIFFSPVSIATAFAM 64
DB 28 QGHVAQETDDTSHQE--AACHKIAPLANPAFSIYHHLAHQSNSTIFFSPVSIASAFAM 85
QY 65 LSLGCTKADTHDEILGLNFNLTPEPAQIHGFGQELLRTLNOPDSOLOLTTGNGLFSE 124
DB 86 LSLGAKGNTETELKUGLGNLTPEPAQIHGFGQELLRTLNOPDSOLOLTTGNGLFSE 145
QY 125 LKLVKDFLEVDKLYHSEAFVNFQGTTEAKKQINDYVEKGTOGKIVDLVKELDRDTVEA 184
DB 146 AKLVDTLEVDKLYHSEAFVNFQGTTEAKKQINDYVEKGTOGKIVDLVKELDRDTVEA 205
QY 185 LVNYIFPKGKWERPFVEKDTVEEDFHVDQVTVTKVPMKRLGMFNTQHCKKLSSWLLMK 244
DB 206 LVNYISFGKWKPFEMKHTERDFHVDQVTVTKVPMKRLGMFNTQHCKKLSSWLLMK 265
QY 245 YLGNTAIFFLPDGKQLHLENELTHDITKFLNEDRRSASLHLFKLSITGYDLKSVL 304
DB 266 YVGNVTACFLPDGKQLHLENELTHDITKFLNEDRRSASLHLFKLSITGYDLKSVL 325
QY 305 GQLGCTKADTHDEILGLNFNLTPEPAQIHGFGQELLRTLNOPDSOLOLTTGNGLFSE 364
DB 326 GDVGITVFSRDLADSGITKEQFLKSVKALHKAALTIKDEKGTAVGSTFEALPMSLPD 385
QY 365 VKFNKPFVFLMIEQNTKSPLEMGKVVNPTQ 394
DB 386 VEFNRPFICILYDRNTKSPLEMGKVVNPTQ 415
PRT; 413 AA.
RESULT 9
ALST_TAMSI STANDARD; PRT; 413 AA.
AC 054759;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1-antitrypsin-like protein CM55-ST precursor.
OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamias.
OX NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alpha1-antitrypsin-like genes in hibernating
RT species of the squirrel family.";
RL Gene 204:127-132(1997).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANTITRYPSIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB000548; BAA24418.1; -.
CC HSP: P01009; 9AP1.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART: SM00093; SERPIN; 1.
CC PROSITE: PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 24
FT ACT_SITE 25 413
FT REACTIVE_BOND.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
FT ACT_SITE 377 378 REACTIVE_BOND (BY SIMILARITY).
FT SEQUENCE 413 AA; 46151 MW; 7A04BFD5C520A55A CRC64;
Query Match 52.0%; Score 1392; DB 1; Length 413;
Best Local Similarity 68.2%; Pred. No. 1.3e-82;
Matches 264; Conservative 59; Mismatches 64; Indels 0; Gaps 0;
QY 9 AQKDTSHDDQDHPFNKTPNLAEPFSLYROLAHQSNSTIFFSPVSIATAFAMLSIG 68
DB 27 AQETEASKQDQHPASHRIAPHLAEFALSFYRLARQSNSTIFFSPVSIATAMLSIG 86
QY 69 TKADYTHDELLEGLNFNLTPEPAQIHGFGQELLRTLNOPDSOLOLTTGNGLFSEGLKLV 128
DB 87 TKGDYTHDELLEGLNFNLTPEPAQIHGFGQELLRTLNOPDSOLOLTTGNGLFSEGLKLV 146
QY 129 DKFLEDVKLYHSEAFVNFQGTTEAKKQINDYVEKGTOGKIVDLVKELDRDTVEFALVNY 188
DB 147 DKFLEDVKLYHSEAFVNFQGTTEAKKQINDYVEKGTOGKIVDLVKELDRDTVEFALVNY 206
QY 189 IFFKKGWERPFVEKDTVEEDFHVDQVTVTKVPMKRLGMFNTQHCKKLSSWLLMKYLG 248
DB 189 IFFKKGWERPFVEKDTVEEDFHVDQVTVTKVPMKRLGMFNTQHCKKLSSWLLMKYLG 248
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Mon Dec 9 12:50:47 2002

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Db 207 IFFKGKWKQPFNEEQTRKDFHVDKATTVVPMNRLGFMHLHHCSTLASVWLQMDYLG 266
QY 249 ATAIFLDPDEGLQHLNETHDITTKFLENEDRRSASLHLPKLSITGYDLSKSVLGQLG 308
Db 267 ATAIFLDPDGKQKQHLNETHDITTKFLENEDRRSASLHLPKLSITGYDLSKSVLGQLG 326
QY 309 ITKVSFSGADLSGVTGTEAPLKLKAVHKAVALTIDKGTGAAGAMFLEAPMSPVPEKFN 368
Db 327 ITKVSFSGADLSGVTGTEAPLKLKAVHKAVALTIDKGTGAAGAMFLEAPMSPVPEKFN 386
QY 369 KPFVFLMIEONTKSPFMGKVVNPTQK 395
Db 387 RPFVLVYIEHHTKSPFLVGVKNVPTQK 413

RESULT 10
ALMS_TAMSI
ID ALMS_TAMSI STANDARD; PRT; 413 AA.
AC 054760;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Alpha-1-antitrypsin-like protein CM55-SI precursor.
OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamias.
OX NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANTITRYPSIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB000549; BAA24419.1; -
CC HSP; P01009; 9API.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART: SM00093; SERPIN; 1.
CC PROSITE: PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 413
FT MOD_RES 25 25
FT CARBOHYD 102 102
FT CARBOHYD 165 165
FT CARBOHYD 266 266
FT ACT_SITE 377 378
FT REACTIVE_BOND (BY SIMILARITY).
SQ SEQUENCE 413 AA; 46202 MW; AB65A1D31B8CA2EC CRC64;

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Query Match 51.9%; Score 1388; DB 1; Length 413;
 Best Local Similarity 68.2%; Pred. No. 2.3e-82;
 Matches 264; Conservative 59; Mismatches 64; Indels 0; Gaps 0;

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QY 9 AOKTDTSHDQDHPTFNKTPNLAFAFSLYRQLAQHSNSTNIFSPVSIATAFAMLSLG 68
Db 27 AQETASKQDQHPASHKTIAPHLAEFALSFYRVLARQSNNTNIFSPVSIATAFAMLSLG 86

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QY 69 TKADTHDEILEGNFLNLTPEAQIHEGFQELLRTLNQPSQLQTLTNGFLSEGLKLV 128
Db 87 TKGDTHDTLLEGLDNFLNLTPEAQIHEGFQELLRTLNQPSQLQTLTNGFLSEGLKLV 146
QY 129 DKFLEDVKKLYHSEAFVNFQDTEAKKQINDYVEKGQKIVDLVKELDRDTFVALVNY 188
Db 147 DKFLEDVKKLYHSEAFVNFQDTEAKKQINDYVEKGQKIVDLVKELDRDTFVALVNY 206
QY 189 IFFKGKWKQPFNEEQTRKDFHVDKATTVVPMNRLGFMHLHHCSTLASVWLQMDYLG 248
Db 207 IFFKGKWKQPFNEEQTRKDFHVDKATTVVPMNRLGFMHLHHCSTLASVWLQMDYLG 266
QY 249 ATAIFLDPDEGLQHLNETHDITTKFLENEDRRSASLHLPKLSITGYDLSKSVLGQLG 308
Db 267 ATAIFLDPDGKQKQHLNETHDITTKFLENEDRRSASLHLPKLSITGYDLSKSVLGQLG 326
QY 309 ITKVSFSGADLSGVTGTEAPLKLKAVHKAVALTIDKGTGAAGAMFLEAPMSPVPEKFN 368
Db 327 ITKVSFSGADLSGVTGTEAPLKLKAVHKAVALTIDKGTGAAGAMFLEAPMSPVPEKFN 386
QY 369 KPFVFLMIEONTKSPFMGKVVNPTQK 395
Db 387 RPFVLVYIEHHTKSPFLVGVKNVPTQK 413

RESULT 11
ALMS_TAMSI
ID ALMS_TAMSI STANDARD; PRT; 413 AA.
AC 054758;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Alpha-1-antitrypsin-like protein CM55-MS precursor.
OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamias.
OX NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANTITRYPSIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB000547; BAA24417.1; -
CC HSP; P01009; 1QLP.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART: SM00093; SERPIN; 1.
CC PROSITE: PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 413
FT MOD_RES 25 25
FT CARBOHYD 65 65
FT CARBOHYD 102 102
FT CARBOHYD 165 165
FT REACTIVE_BOND (BY SIMILARITY).
SQ SEQUENCE 413 AA; 46202 MW; AB65A1D31B8CA2EC CRC64;

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FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 413 AA: 45952 MW: 430374CA26EBAF08 CRC64;

Query Match 51.4%; Score 1376; DB 1; Length 413;
Best Local Similarity 68.7%; Pred. No. 1.4e-81;
Matches 266; Conservative 53; Mismatches 68; Indels 0; Gaps 0;

QY 9 AQKTDTHSHDQDHTNKNTPNLAFAFSLYROLAHSNSTNFFSPVSIATAFAMLSG 68
DB 27 AQETASKQDQEPASHRIAPHIAEAFSLYRLARQSNNTNFFSPVSIATAFAMLSG 86
QY 69 TKADTHDEILEGNFNLTETPEAQIHGEGFOELLRTLNQPSQLQTLTGNGLFSEGLK 128
DB 87 TKGDTHQILEGLDFNLTEMAEADIHQGFQHLLOTLNRPNTQLTSGNGLFTHQNLKLL 146
QY 129 DKFLEDVKLYHSEAFVNFQDTEEAQKQINDYVEGTQKIVDLVKELDRDVFALVNY 188
DB 147 DKFLEDVKLYHSEAFVNFQDTEEAQKQINDYVEGTQKIVDLVKELDRDVFALVNY 206
QY 189 IFFKQKWERPEVKDTEEDFHVDOVTVKVPMMKRLGFNIHQCKLSWVLLMKYLG 248
DB 207 IFFKQKWERPEVKDTEEDFHVDOVTVKVPMMKRLGFNIHQCKLSWVLLMKYLG 266
QY 249 ATAFIFLPDQKQHLNLTETPEAQIHGEGFOELLRTLNQPSQLQTLTGNGLFSEGLK 308
DB 267 ATAFIFLPDQKQHLNLTETPEAQIHGEGFOELLRTLNQPSQLQTLTGNGLFSEGLK 326
QY 309 ITRVFSNGADLSGVTEAPKLSKAVHKAVLTIDEGTGAAGAMFLEAIPMSIPPEVK 368
DB 327 ITRVFSNGADLSGVTEAPKLSKAVHKAVLTIDEGTGAAGAMFLEAIPMSIPPEVK 386
QY 369 KPFVFLMIEQNTKSPFLPMGKVVNPTQK 395
DB 387 RPLVFLVYIHHKTSPLFVGKVVNPTQK 413

RESULT 12
ALAF_RABIT
ID ALAF_RABIT STANDARD; PRT; 413 AA.
AC P23035;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Alpha-1-antitrypsin F precursor (Alpha-1-antitrypsin) (Alpha-1-
DE protease inhibitor) (APF).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91201273; PubMed=2016265;
RA Saito A., Sinohara H.;
RT "Cloning and sequencing of cDNA coding for rabbit alpha-1-
RT antitrypsinase F: amino acid sequence comparison of alpha-1-
RT antitrypsinase of six mammals.";
RL J. Biochem. 109:158-162(1991).
RN [2]
RP SEQUENCE OF 25-41.
RX MEDLINE=88227895; PubMed=3259574;
RA Saito A., Sinohara H.;
RT "Differential interactions of rabbit plasma alpha-1-antitrypsinases S
RT and F with porcine trypsin.";
RL J. Biochem. 103:247-253(1988).
RN [3]
RP SEQUENCE OF 374-380.
RX MEDLINE=91035333; PubMed=2229014;
RA Saito A., Sinohara H.;
RT "Amino acid sequence at the reactive site of rabbit alpha-1-
RT antitrypsinases.";
RL J. Biochem. 108:80-85(1990).
CC -|- FUNCTION: INHIBITOR OF SERINE PROTEASES. THE PRIMARY TARGET IS
```

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CC ELASTASE, BUT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
CC THROMBIN.
CC -|- SUBCELLULAR LOCATION: Extracellular.
CC -|- TISSUE SPECIFICITY: PLASMA.
CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC -----
CC EMBL: X57710; CAA40881.1; -.
CC EMBL: D00853; BAA00728.1; -.
CC PIR: JX0154; JX0154.
CC HSSP: P01009; 8AP1.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART: SM00093; SERPIN; 1.
CC PROSITE: PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
FT SIGNAL 1 24
FT CHAIN 25 413 ALPHA-1-ANTITRYPSINASE F.
FT ACT_SITE 377 378 REACTIVE BOND.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 413 AA: 45867 MW: E851F5DE63A592DF CRC64;

Query Match 50.0%; Score 1338; DB 1; Length 413;
Best Local Similarity 64.9%; Pred. No. 3.8e-79;
Matches 252; Conservative 62; Mismatches 74; Indels 0; Gaps 0;

QY 7 DAAQKTDTSHDQDHTNKNTPNLAFAFSLYROLAHSNSTNFFSPVSIATAFAMLS 66
DB 25 DEAQETAVSSHEQDHPACHRTAPSLAEFALSILYREVAHESNTNFFSPVSIATAFAMLS 84
QY 67 LGTKADTHDEILEGNFNLTETPEAQIHGEGFOELLRTLNQPSQLQTLTGNGLFSEGLK 126
DB 85 LGCAKGDTHQVLEGLKFNLTETAEQIHGDFPHLLTNNRPDSELQLAARNALVYHENLK 144
QY 127 LVDFLEDDVKLYHSEAFVNFQDTEEAQKQINDYVEGTQKIVDLVKELDRDVFALV 186
DB 145 LQHKLEDAKNDYQSEAFVNFQDTEEAQKQINDYVEGTQKIVDLVKELDRDVFALV 204
QY 187 NVIFFKQKWERPEVKDTEEDFHVDOVTVKVPMMKRLGFNIHQCKLSWVLLMKYL 246
DB 205 NVIFFKQKWERPEVKDTEEDFHVDOVTVKVPMMKRLGFNIHQCKLSWVLLMKYL 264
QY 247 GNATAIFFLPDQKQHLNLTETPEAQIHGEGFOELLRTLNQPSQLQTLTGNGLFSEGLK 306
DB 265 GNATAIFFLPDQKQHLNLTETPEAQIHGEGFOELLRTLNQPSQLQTLTGNGLFSEGLK 324
QY 307 LGITVFSNGADLSGVTEAPKLSKAVHKAVLTIDEGTGAAGAMFLEAIPMSIPPEVK 366
DB 325 LGITVFSNGADLSGVTEAPKLSKAVHKAVLTIDEGTGAAGAMFLEAIPMSIPPEVK 384
QY 367 KPFVFLMIEQNTKSPFLPMGKVVNPTQK 394
DB 385 RPLVFLVYIHHKTSPLFVGKVVNPTQK 412

RESULT 13
ALAF_MOUSE
ID ALAF_MOUSE STANDARD; PRT; 413 AA.
AC P07758;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-1-antitrypsin 1-1 precursor (Serine protease inhibitor 1-1)
```

(Alpha-1 protease inhibitor 1) (Alpha-1-antitrypsinase) (AAT).
 Sp11-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=92052104; PubMed=1946354;
 RA Borriello F., Krauter K.S.;
 RT "Multiple murine alpha 1-protease inhibitor genes show unusual
 evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
 RN [2]
 RP SEQUENCE OF 211-413 FROM N.A.
 RX MEDLINE=86163765; PubMed=3007061;
 RA Krauter K.S., Citron B.A., Hsu M.T., Powell D., Darnell J.E. Jr.;
 RT "Isolation and characterization of the alpha 1-antitrypsin gene of
 mice.";
 RL DNA 5:29-36(1986).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES, ITS PRIMARY TARGET IS
 ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 THROMBIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M75721; AAC28869.1; -;
 DR EMBL; M12586; AAA51624.1; -;
 DR PIR; A25495; A25495.
 DR HSP; P01009; 8AP1.
 DR MGD; MGI:891971; Sp11-1.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 KW Multigene family.
 FT SIGNAL 1 24
 FT CHAIN 25 413
 FT ACT_SITE 377 378
 FT CARBOHYD 64 64
 FT CARBOHYD 101 101
 FT CARBOHYD 265 265
 FT CONFLICT 246 246
 FT CONFLICT 323 323
 FT CONFLICT 404 404
 FT SEQUENCE 413 AA; 46002 MW; 1124B2CC356232F4 CRC64;
 Query Match 49.9%; Score 1335; DB 1; Length 413;
 Best Local Similarity 64.3%; Pred. No. 6e-79;
 Matches 249; Conservative 70; Mismatches 66; Indels 2; Gaps 2;
 QY 10 QKTDTHDQDPTNKTPNLAERAFSLYRLQAHQSNSTIFFSPVSIATAFAMLSLGT 69
 DB 28 QETDTSQKDDQ-PASHEIATNLGDFAISLYRELHVQSNSTIFFSPVSIATAFAMLSLGS 86
 QY 70 KADTHDEILEGLNLFNLTPEAQHEGFQELLRTLNQDPSQLQTLTGNGFLSEGLKLV 129
 DB 87 KGDTHQILEGLQFNLTQTSADTHKSFQHLQTLNRPDSQLQTLTGNGFLVNDKLV 146
 QY 130 KFLVDKLYLSEAFVNFVGTGTEAKKQINDYVEKGTQKIVDLVKELDRDVFALVNYI 189
 DB 147 KFLSEAKNHYQAEVSVNFAESEAKKVINDFVEKGTQKIAEAVKQLDQTVFALANYI 206
 QY 190 PFKGWERPFVEKDTDEEDFHVQDVTTKVPMKRLGMFNTHQCKKLSSVLLMKYLGN 249

DB 207 LFKGKKKPPDPNTEAEAFHVDSTTKVPMNTLSGMLRHVHCSTLSSVLLMDYAGNA 266
 QY 250 TATFELPDECKLOHLENELTHDIIITKPLENEDRRSSASLHLPKLSITGTVDLKSVLGOLGI 309
 DB 267 TAVFLPDDCKMOHLEQTLSEKLSIFLLNRRRLAQIHFPRLSISGEYNLKTMSPLGI 326
 QY 310 TKVFSNGADLSGVTEE-APLKLSKAVHKAVLTITDERKTEAAGAMFLEAIPMSIPPEVKFN 368
 DB 327 TRIFNNGADLSGITEENAPLKLSQAVHKAVLTITDEGTAAAVTVLQWVPMSPILRED 386
 QY 369 KPFFVLMIEQNTSKPLPMGKVNPOTOK 395
 DB 387 HPFLFIIEEHTQSPIFLGRKVDPTHK 413
 RESULT 14
 ALT2_MOUSE
 ID ALT2_MOUSE STANDARD; PRT; 413 AA.
 AC P22599; Q61283;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin 1-2 precursor (Serine protease inhibitor 1-2)
 GN SP11-2 OR AAT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90152670; PubMed=2303252;
 RA Sifers R.N., Ledley F.D., Reed-Fourquet L., Ledbetter D.H.;
 RA Ledbetter S.A., Woo S.L.C.;
 RT "Complete cDNA sequence and chromosomal localization of mouse alpha
 1-antitrypsin.";
 RL Genomics 6:100-104(1990).
 RN [2]
 RP SEQUENCE OF 12-413 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=92052104; PubMed=1946354;
 RA Borriello F., Krauter K.S.;
 RT "Multiple murine alpha 1-protease inhibitor genes show unusual
 evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 THROMBIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M25529; AAA37132.1; -;
 DR EMBL; M75716; AAC28865.1; -;
 DR HSP; P01009; 8AP1.
 DR MGD; MGI:891970; Sp11-2.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 KW Multigene family.
 FT SIGNAL 1 24
 FT CHAIN 25 413
 FT ACT_SITE 377 378
 FT ACT_SITE 377 378
 FT CARBOHYD 64 64
 FT CARBOHYD 101 101
 FT CARBOHYD 265 265
 FT CONFLICT 246 246
 FT CONFLICT 323 323
 FT CONFLICT 404 404
 FT SEQUENCE 413 AA; 46002 MW; 1124B2CC356232F4 CRC64;
 Query Match 49.9%; Score 1335; DB 1; Length 413;
 Best Local Similarity 64.3%; Pred. No. 6e-79;
 Matches 249; Conservative 70; Mismatches 66; Indels 2; Gaps 2;
 QY 10 QKTDTHDQDPTNKTPNLAERAFSLYRLQAHQSNSTIFFSPVSIATAFAMLSLGT 69
 DB 28 QETDTSQKDDQ-PASHEIATNLGDFAISLYRELHVQSNSTIFFSPVSIATAFAMLSLGS 86
 QY 70 KADTHDEILEGLNLFNLTPEAQHEGFQELLRTLNQDPSQLQTLTGNGFLSEGLKLV 129
 DB 87 KGDTHQILEGLQFNLTQTSADTHKSFQHLQTLNRPDSQLQTLTGNGFLVNDKLV 146
 QY 130 KFLVDKLYLSEAFVNFVGTGTEAKKQINDYVEKGTQKIVDLVKELDRDVFALVNYI 189
 DB 147 KFLSEAKNHYQAEVSVNFAESEAKKVINDFVEKGTQKIAEAVKQLDQTVFALANYI 206
 QY 190 PFKGWERPFVEKDTDEEDFHVQDVTTKVPMKRLGMFNTHQCKKLSSVLLMKYLGN 249

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CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL: M75720; AAC28868.1; --	
DR	HSSP: P01009; 9AP1.	
DR	MGD: MGI:891969; Sp11-3.	
DR	InterPro: IPR000215; Serpin.	
DR	Pfam: PF00079; serpin; 1.	
DR	SMART: SM00093; SERPIN; 1.	
DR	PROSITE: PS00284; SERPIN; 1.	
DR	Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;	
KW	Multigene family.	
FT	SIGNAL	1 24
FT	CHAIN	25 413
FT	ACT_SITE	377 378
FT	CARBOHYD	64 101
FT	CARBOHYD	101 101
FT	CARBOHYD	265 265
FT	SEQUENCE	413 AA; 45854 MW; 7EAD710919A1C5B CRC64;
SO		
	POTENTIAL.	
	ALPHA-1-ANTITRYPSIN 1-3.	
	REACTIVE_BOND (BY SIMILARITY).	
	N-LINKED (GLCNAC. . .) (POTENTIAL).	
	N-LINKED (GLCNAC. . .) (POTENTIAL).	
	N-LINKED (GLCNAC. . .) (POTENTIAL).	

	QY	250	TALFFDDEGKQLHLENELTHDIITFLENEEDRRKSASLRLPKPLSTGTULDKSLVWGUGLI	309
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	Dd	267	TAVELLPPDDCKMHLQETLSKEITSFKLLRPRRLAQIHFPRLISGSYEKLTKMLSPGI	326
			::: ::: ::: ::: ::: ::: :::	
	QY	310	TKVFSCNGADLSGVTEE-APUKLKSAVKHKAVLTIDEKTEAAGAMFLGAIPMSIPEPVKEN	368
			::: ::: ::: ::: ::: ::: :::	
	Dd	327	TRIFNCGADLSGVTEENAPUKLKSAVKHKAVLTIDETGETEAANATVLVAVPYSMPPIVRFD	386
			::: ::: ::: ::: ::: ::: :::	
	QY	369	KPFVFLMIEQNTKSPLFMGKVKNPTQK	395
			::: ::: ::: ::: ::: ::: :::	
	Dd	387	HPFLFIIFEHTQSPLFVGKVDPTKH	413

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